



RAW SEQUENCE LISTING ERROR REPORT

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: 09/733,773A

Source: OIR

Date Processed by STIC: 6/20/2001

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.

PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:

- 1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,
- 2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY

FOR CRF SUBMISSION QUESTIONS, PLEASE CONTACT MARK SPENCER, 703-308-4212.

FOR SEQUENCE RULES INTERPRETATION, PLEASE CONTACT ROBERT WAX, 703-308-4216.

PATENTIN 2.1 e-mail help: patin21help@uspto.gov or phone 703-306-4119 (R. Wax)

PATENTIN 3.0 e-mail help: patin3help@uspto.gov or phone 703-306-4119 (R. Wax)

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE CHECKER VERSION 3.0 PROGRAM, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW:

Checker Version 3.0

The Checker Version 3.0 application is a state-of-the-art Windows based software program employing a logical and intuitive user-interface to check whether a sequence listing is in compliance with format and content rules. Checker Version 3.0 works for sequence listings generated for the original version of 37 CFR §§1.821 - 1.825 effective October 1, 1990 (old rules) and the revised version (new rules) effective July 1, 1998 as well as World Intellectual Property Organization (WIPO) Standard ST.25.

Checker Version 3.0 replaces the previous DOS-based version of Checker, and is Y2K-compliant. Checker allows public users to check sequence listings in Computer Readable form (CRF) before submitting them to the United States Patent and Trademark Office (USPTO). Use of Checker prior to filing the sequence listing is expected to result in fewer errored sequence listings, thus saving time and money.

Checker Version 3.0 can be down loaded from the USPTO website at the following address:

<http://www.uspto.gov/web/offices/pac/checker>

Raw Sequence Listing Error Summary

ERROR DETECTED SUGGESTED CORRECTION

SERIAL NUMBER: 09/233,773

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

- 1 Wrapped Nucleics The number/text at the end of each line "wrapped" down to the next line.
This may occur if your file was retrieved in a word processor after creating it.
Please adjust your right margin to .3, as this will prevent "wrapping".
- 2 Wrapped Aminos The amino acid number/text at the end of each line "wrapped" down to the next line.
This may occur if your file was retrieved in a word processor after creating it.
Please adjust your right margin to .3, as this will prevent "wrapping".
- 3 Incorrect Line Length The rules require that a line not exceed 72 characters in length. This includes spaces.
- 4 Misaligned Amino Acid Numbering The numbering under each 5th amino acid is misaligned. This may be caused by the use of tabs between the numbering. It is recommended to delete any tabs and use spacing between the numbers.
- 5 Non-ASCII This file was not saved in ASCII (DOS) text, as required by the Sequence Rules.
Please ensure your subsequent submission is saved in ASCII text so that it can be processed.
- 6 Variable Length Sequence(s) contain n's or Xaa's which represented more than one residue.
As per the rules, each n or Xaa can only represent a single residue.
Please present the maximum number of each residue having variable length and indicate in the (ix) feature section that some may be missing.
- 7 PatentIn ver. 2.0 "bug" A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequence(s) . Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. This applies primarily to the mandatory <220>-<223> sections for Artificial or Unknown sequences.
- 8 Skipped Sequences (OLD RULES) Sequence(s) missing. If intentional, please use the following format for each skipped sequence:
(2) INFORMATION FOR SEQ ID NO:X:
(i) SEQUENCE CHARACTERISTICS:(Do not insert any headings under "SEQUENCE CHARACTERISTICS")
(xi) SEQUENCE DESCRIPTION:SEQ ID NO:X:
This sequence is intentionally skipped

Please also adjust the "(iii) NUMBER OF SEQUENCES:" response to include the skipped sequence(s).
- 9 Skipped Sequences (NEW RULES) Sequence(s) missing. If intentional, please use the following format for each skipped sequence.
<210> sequence id number
<400> sequence id number
000
- 10 Use of n's or Xaa's (NEW RULES) Use of n's and/or Xaa's have been detected in the Sequence Listing.
Use of <220> to <223> is MANDATORY if n's or Xaa's are present.
In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represent.
- 11 Use of <213>Organism (NEW RULES) Sequence(s) are missing this mandatory field or its response.
- 12 Use of <220>Feature (NEW RULES) Sequence(s) are missing the <220>Feature and associated headings.
Use of <220> to <223> is MANDATORY if <213>ORGANISM is "Artificial" or "Unknown".
Please explain source of genetic material in <220> to <223> section.
(See "Federal Register," 6/01/98, Vol. 63, No. 104, pp. 29631-32) *new Rules*
- 13 PatentIn ver. 2.0 "bug" Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes the file, resulting in missing mandatory numeric identifiers and responses (as indicated). Instead, please use "File Manager" or any other means to copy file to floppy disk.

OIPE

RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/733,773A

DATE: 06/20/2001

TIME: 14:37:16

Input Set : A:\SALK2410.ST25.txt

Output Set: N:\CRF3\06202001\I733773A.raw

Does Not Comply
Corrected Diskette Needed
m. 2-3,5

3 <110> APPLICANT: The Salk Institute For Biological Studies
4 NOEL, Joseph
5 VERDECIA, Mark
7 <120> TITLE OF INVENTION: CRYSTAL STRUCTURE OF WW DOMAINS AND METHODS AND USE THEREOF
9 <130> FILE REFERENCE: SALK2410
11 <140> CURRENT APPLICATION NUMBER: US 09/733,773A
C--> 12 <141> CURRENT FILING DATE: 2001-06-04
14 <160> NUMBER OF SEQ ID NOS: 32
16 <170> SOFTWARE: PatentIn version 3.0
18 <210> SEQ ID NO: 1
19 <211> LENGTH: 163
20 <212> TYPE: PRT
21 <213> ORGANISM: Homo sapiens
23 <220> FEATURE:
24 <221> NAME/KEY: PEPTIDE
25 <222> LOCATION: (1)..(163)
26 <223> OTHER INFORMATION: Pin1
28 <400> SEQUENCE: 1
30 Met Ala Asp Glu Glu Lys Leu Pro Pro Gly Trp Glu Lys Arg Met Ser
31 1 5 10 15
33 Arg Ser Ser Gly Arg Val Tyr Tyr Phe Asn His Ile Thr Asn Ala Ser
34 20 25 30
36 Gln Trp Glu Arg Pro Ser Gly Asn Ser Ser Ser Gly Gly Lys Asn Gly
37 35 40 45
39 Gln Gly Glu Pro Ala Arg Val Arg Cys Ser His Leu Leu Val Lys His
40 50 55 60
42 Ser Gln Ser Arg Arg Pro Ser Ser Trp Arg Gln Glu Lys Ile Thr Arg
43 65 70 75 80
45 Thr Lys Glu Glu Ala Leu Glu Leu Ile Asn Gly Tyr Ile Gln Lys Ile
46 85 90 95
48 Lys Ser Gly Glu Glu Asp Phe Glu Ser Leu Ala Ser Gln Phe Ser Asp
49 100 105 110
51 Cys Ser Ser Ala Lys Ala Arg Gly Asp Leu Gly Ala Phe Ser Arg Gly
52 115 120 125
54 Gln Met Gln Lys Pro Phe Glu Asp Ala Ser Phe Ala Leu Arg Thr Gly
55 130 135 140
57 Glu Met Ser Gly Pro Val Phe Thr Asp Ser Gly Ile His Ile Ile Leu
58 145 150 155 160
60 Arg Thr Glu
63 <210> SEQ ID NO: 2
64 <211> LENGTH: 38
65 <212> TYPE: PRT
66 <213> ORGANISM: Homo sapiens
68 <220> FEATURE:
69 <221> NAME/KEY: DOMAIN
70 <222> LOCATION: (1)..(38)
71 <223> OTHER INFORMATION: Ww Domain of Pin1

RAW SEQUENCE LISTING
PATENT APPLICATION: US/09/733,773A

DATE: 06/20/2001
TIME: 14:37:16

Input Set : A:\SALK2410.ST25.txt
Output Set: N:\CRF3\06202001\I733773A.raw

73 <400> SEQUENCE: 2
75 Met Ala Asp Glu Glu Lys Leu Pro Pro Gly Trp Glu Lys Arg Met Ser
76 1 5 10 15
78 Arg Ser Ser Gly Arg Val Tyr Tyr Phe Asn His Ile Thr Asn Ala Ser
79 20 25 30
81 Gln Trp Glu Arg Pro Ser
82 35
84 <210> SEQ ID NO: 3
85 <211> LENGTH: 7
86 <212> TYPE: PRT
87 <213> ORGANISM: Homo sapiens
89 <220> FEATURE:
90 <221> NAME/KEY: MOD_RES
91 <222> LOCATION: (2)..(2)
92 <223> OTHER INFORMATION: PHOSPHORYLATION
94 <220> FEATURE:
95 <221> NAME/KEY: MOD_RES
96 <222> LOCATION: (5)..(5)
97 <223> OTHER INFORMATION: PHOSPHORYLATION
99 <400> SEQUENCE: 3
101 Tyr Ser Pro Thr Ser Pro Ser
102 1 5
104 <210> SEQ ID NO: 4
105 <211> LENGTH: 9
106 <212> TYPE: PRT
108 <213> ORGANISM: ARTIFICIAL
109 <220> FEATURE:
110 <223> OTHER INFORMATION: PEPTIDE
W--> 112 <220> FEATURE:
113 <221> NAME/KEY: VARIANT
114 <222> LOCATION: (6)..(6)
115 <223> OTHER INFORMATION: Xaa is any amino acid (Pro in Figure 4a & 4b)
117 <400> SEQUENCE: 4
W 119 Gly Thr Pro Pro Pro Xaa Tyr Thr Val
120 1 5
122 <210> SEQ ID NO: 5
123 <211> LENGTH: 8
124 <212> TYPE: PRT
125 <213> ORGANISM: ARTIFICIAL
127 <220> FEATURE:
128 <223> OTHER INFORMATION: Peptide
130 <400> SEQUENCE: 5
132 Trp Phe Tyr Ser Pro Phe Leu Glu
133 1 5
135 <210> SEQ ID NO: 6
136 <211> LENGTH: 8
137 <212> TYPE: PRT
138 <213> ORGANISM: ARTIFICIAL
140 <220> FEATURE:

insufficient exploration - give source of genetic material (see item 11 on summary sheet)

Error summary sheet)

RAW SEQUENCE LISTING
PATENT APPLICATION: US/09/733,773A

DATE: 06/20/2001
TIME: 14:37:16

Input Set : A:\SALK2410.ST25.txt
Output Set: N:\CRF3\06202001\I733773A.raw

141 <223> OTHER INFORMATION: Peptide
143 <220> FEATURE:
144 <221> NAME/KEY: MOD_RES
145 <222> LOCATION: (4)..(4)
146 <223> OTHER INFORMATION: PHOSPHORYLATION
148 <400> SEQUENCE: 6
150 Trp Phe Tyr Ser Pro Phe Leu Glu
151 1 5
153 <210> SEQ ID NO: 7
154 <211> LENGTH: 6
155 <212> TYPE: PRT
156 <213> ORGANISM: Homo sapiens
158 <220> FEATURE:
159 <221> NAME/KEY: MOD_RES
160 <222> LOCATION: (4)..(4)
161 <223> OTHER INFORMATION: PHOSPHORYLATION
163 <400> SEQUENCE: 7
165 Val Pro Arg Thr Pro Val
166 1 5
168 <210> SEQ ID NO: 8
169 <211> LENGTH: 6
170 <212> TYPE: PRT
171 <213> ORGANISM: Homo sapiens
173 <220> FEATURE:
174 <221> NAME/KEY: MOD_RES
175 <222> LOCATION: (4)..(4)
176 <223> OTHER INFORMATION: PHOSPHORYLATION
178 <400> SEQUENCE: 8
180 Tyr Leu Gly Ser Pro Ile
181 1 5
183 <210> SEQ ID NO: 9
184 <211> LENGTH: 6
185 <212> TYPE: PRT
186 <213> ORGANISM: Homo sapiens
188 <220> FEATURE:
189 <221> NAME/KEY: MOD_RES
190 <222> LOCATION: (4)..(4)
191 <223> OTHER INFORMATION: PHOSPHORYLATION
193 <400> SEQUENCE: 9
195 Leu Tyr Arg Ser Pro Ser
196 1 5
198 <210> SEQ ID NO: 10
199 <211> LENGTH: 6
200 <212> TYPE: PRT
201 <213> ORGANISM: Homo sapiens
203 <220> FEATURE:
204 <221> NAME/KEY: MOD_RES
205 <222> LOCATION: (4)..(4)
206 <223> OTHER INFORMATION: PHOSPHORYLATION

RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/733,773A

DATE: 06/20/2001

TIME: 14:37:16

Input Set : A:\SALK2410.ST25.txt

Output Set: N:\CRF3\06202001\I733773A.raw

208 <400> SEQUENCE: 10
210 Gly Ser Ser Ser Pro Val
211 1 5
213 <210> SEQ ID NO: 11
214 <211> LENGTH: 6
215 <212> TYPE: PRT
216 <213> ORGANISM: Homo sapiens
218 <220> FEATURE:
219 <221> NAME/KEY: MOD_RES
220 <222> LOCATION: (4)..(4)
221 <223> OTHER INFORMATION: PHOSPHORYLATION
223 <400> SEQUENCE: 11
225 Pro Pro Ala Thr Pro Pro
226 1 5
228 <210> SEQ ID NO: 12
229 <211> LENGTH: 6
230 <212> TYPE: PRT
231 <213> ORGANISM: Homo sapiens
233 <220> FEATURE:
234 <221> NAME/KEY: MOD_RES
235 <222> LOCATION: (4)..(4)
236 <223> OTHER INFORMATION: PHOSPHORYLATION
238 <400> SEQUENCE: 12
240 Pro Pro Gly Ser Pro Pro
241 1 5
243 <210> SEQ ID NO: 13
244 <211> LENGTH: 6
245 <212> TYPE: PRT
246 <213> ORGANISM: Homo sapiens
248 <220> FEATURE:
249 <221> NAME/KEY: MOD_RES
250 <222> LOCATION: (4)..(4)
251 <223> OTHER INFORMATION: PHOSPHORYLATION
253 <400> SEQUENCE: 13
255 Ser Thr Ser Thr Pro Arg
256 1 5
258 <210> SEQ ID NO: 14
259 <211> LENGTH: 7
260 <212> TYPE: PRT
261 <213> ORGANISM: Homo sapiens
263 <400> SEQUENCE: 14
265 Tyr Ser Pro Thr Ser Pro Ser
266 1 5
268 <210> SEQ ID NO: 15
269 <211> LENGTH: 7
270 <212> TYPE: PRT
271 <213> ORGANISM: Homo sapiens
273 <220> FEATURE:
274 <221> NAME/KEY: MOD_RES

RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/733,773A

DATE: 06/20/2001

TIME: 14:37:16

Input Set : A:\SALK2410.ST25.txt

Output Set: N:\CRF3\06202001\I733773A.raw

275 <222> LOCATION: (2)..(2)
 276 <223> OTHER INFORMATION: PHOSPHORYLATION
 278 <400> SEQUENCE: 15
 280 Tyr Ser Pro Thr Ser Pro Ser
 281 1 5
 283 <210> SEQ ID NO: 16
 284 <211> LENGTH: 7
 285 <212> TYPE: PRT
 286 <213> ORGANISM: Homo sapiens
 288 <220> FEATURE:
 289 <221> NAME/KEY: MOD_RES
 290 <222> LOCATION: (5)..(5)
 291 <223> OTHER INFORMATION: PHOSPHORYLATION
 293 <400> SEQUENCE: 16
 295 Tyr Ser Pro Thr Ser Pro Ser
 296 1 5
 298 <210> SEQ ID NO: 17
 299 <211> LENGTH: 7
 300 <212> TYPE: PRT
 301 <213> ORGANISM: Homo sapiens
 303 <220> FEATURE:
 304 <221> NAME/KEY: MOD_RES
 305 <222> LOCATION: (2)..(2)
 306 <223> OTHER INFORMATION: PHOSPHORYLATION
 308 <220> FEATURE:
 309 <221> NAME/KEY: MOD_RES
 310 <222> LOCATION: (5)..(5)
 311 <223> OTHER INFORMATION: PHOSPHORYLATION
 313 <400> SEQUENCE: 17
 315 Tyr Ser Pro Thr Ser Pro Ser
 316 1 5
 318 <210> SEQ ID NO: 18
 319 <211> LENGTH: 34
 320 <212> TYPE: PRT
 C--> 321 <213> ORGANISM: ARTIFICIAL
 323 <220> FEATURE:
 324 <223> OTHER INFORMATION: PEPTIDE *see item 11*
 326 <400> SEQUENCE: 18
 328 Lys Leu Pro Pro Gly Trp Glu Lys Arg Met Ser Arg Ser Ser Gly Arg
 329 1 5 10 15
 331 Val Tyr Tyr Phe Asn His Ile Thr Asn Ala Ser Gln Trp Glu Arg Pro
 332 20 25 30
 334 Ser Gly
 337 <210> SEQ ID NO: 19
 338 <211> LENGTH: 34
 339 <212> TYPE: PRT
 C--> 340 <213> ORGANISM: ARTIFICIAL
 342 <220> FEATURE:
 343 <223> OTHER INFORMATION: PEPTIDE *item 11*

*please correct this
error in subsequent
sequences*

VERIFICATION SUMMARY

PATENT APPLICATION: US/09/733,773A

DATE: 06/20/2001

TIME: 14:37:18

Input Set : A:\SALK2410.ST25.txt

Output Set: N:\CRF3\06202001\I733773A.raw

L:12 M:271 C: Current Filing Date differs, Replaced Current Filing Date
L:108 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:4
L:109 M:283 W: Missing Blank Line separator, <220> field identifier
L:119 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:4
L:125 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:5
L:138 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:6
L:321 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:18
L:340 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:19
L:359 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:20
L:378 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:21
L:397 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:22
L:416 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:23
L:435 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:24
L:454 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:25
L:470 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:26
L:489 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:27
L:508 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:28
L:527 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:29
L:546 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:30
L:565 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:31
L:584 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:32